

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lam, Xanthe M.
Oeswein, James Q.
5 Ongpipattanakul, Boonsri
Shahrokh, Zahra
Wang, Sharon X.
Weissburg, Robert P.
Wong, Rita L.
- 10 (ii) TITLE OF INVENTION: Antibody Formulation
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
25 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/874897
30 (B) FILING DATE: 06/13/1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lee, Wendy M.
(B) REGISTRATION NUMBER: 40,378
(C) REFERENCE/DOCKET NUMBER: P1089R1
- 35 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-1994
(B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
	1				5					10					15	
	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	
					20					25					30	
10	Glu	Tyr	Thr	Met	His	Trp	Met	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
					35					40					45	
	Glu	Trp	Val	Ala	Gly	Ile	Asn	Pro	Lys	Asn	Gly	Gly	Thr	Ser	His	
					50					55					60	
	Asn	Gln	Arg	Phe	Met	Asp	Arg	Phe	Thr	Ile	Ser	Val	Asp	Lys	Ser	
15					65					70					75	
	Thr	Ser	Thr	Ala	Tyr	Met	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
					80					85					90	
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Trp	Arg	Gly	Leu	Asn	Tyr	Gly	
					95					100					105	
20	Phe	Asp	Val	Arg	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	
					110					115					120	
	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
					125					130					135	
	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	
25					140					145					150	
	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
					155					160					165	
	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
					170					175					180	
30	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
					185					190					195	
	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	
					200					205					210	

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 215 220 225

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 230 235 240

5 Leu
 241

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15

15 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn
 20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45

20 Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 80 85 90

25 Gly Asn Thr Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
 95 100 105

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 110 115 120

30 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 140 145 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu

155

160

165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 170 175 180

5 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 185 190 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 200 205 210

Arg Gly Glu Cys
 214

10 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Gly Gly Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu
 1 5 10 15

Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys
 20 25 30

20 Lys Leu Val Gly Glu Arg
 35 36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 25 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Lys Asn Ser Ser Met Ile Ser Asn Thr Pro
 1 5 10 11

30 (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Gln Ser Leu Gly Thr Gln
1 5 7

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

His Gln Asn Leu Ser Asp Gly Lys
1 5 8

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 His Gln Asn Ile Ser Asp Gly Lys
1 5 8

(2) INFORMATION FOR SEQ ID NO:8:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Ile Ser Ser His Leu Gly Gln
1 5 8

(2) INFORMATION FOR SEQ ID NO:9:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2143 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
TCATTGCTGA GTTGTATTATTT AAGCTTTGGA GATTATCGTC ACTGCAATGC 100
5 TTCGCAATAT GGCACAAAAT GACCAACAGC GGTGATTGA TCAGGTAGAG 150
GGGGCGCTGT ACGAGGTAAA GCCCAGTGCC AGCATTCCTG ACGACGATAC 200
GGAGCTGCTG CGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250
AAAAAGTTAA TCTTTTCAAC AGCTGTCATA AAGTTGTCAC GGCCGAGACT 300
TATAGTCGCT TTGTTTTTAT TTTTAAATGT ATTTGTAAGT AGAATTCGAG 350
10 CTCGCCGGGG ATCCTCTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC 400
GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA 450
CGCTGATATC CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG 500
GCGATAGGGT CACCATCACC TGTCGTGCCA GTCAGGACAT CAACAATTAT 550
CTGAACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA 600
15 CTATACCTCC ACCCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGTTCTG 650
GTTCTGGGAC GGATTACACT CTGACCATCA GCAGTCTGCA ACCGGAGGAC 700
TTCGCAACTT ATTACTGTCA GCAAGGTAAT ACTCTGCCGC CGACGTTCCG 750
ACAGGGCACG AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT 800
TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT 850
20 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA 900
GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC 950
AGGACAGCAA GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC 1000
AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA 1050
GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAG 1100

CTGATCCTCT ACGCCGGACG CATCGTGGCG CTAGTACGCA AGTTCACGTA 1150
 AAAACGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 1200
 TCTTCTTGCA TCTATGTTCTG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 1250
 AGGTTCAGCT GGTGGAGTCT GGC GG TGGCC TGGTGCAGCC AGGGGGCTCA 1300
 5 CTCCGTTTGT CCTGTGCAAC TTCTGGCTAC ACCTTTACCG AATACACTAT 1350
 GCACTGGATG CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGCAGGGA 1400
 TTAATCCTAA AAACGGTGGT ACCAGCCACA ACCAGAGGTT CATGGACCGT 1450
 TTCACTATAA GCGTAGATAA ATCCACCAGT ACAGCCTACA TGCAAATGAA 1500
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTATTGTGCT AGATGGCGAG 1550
 10 GCCTGAACTA CGGCTTTGAC GTCCGTTATT TTGACGTCTG GGGTCAAGGA 1600
 ACCCTGGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CGGTCTTCCC 1650
 CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT 1700
 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 1750
 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC 1800
 15 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG 1850
 GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG 1900
 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACACATGCCC 1950
 GCCGTGCCCC GCACCAGAAC TGCTGGGCGG CCGCATGAAA CAGCTAGAGG 2000
 ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG 2050
 20 GCAAGACTCA AAAAGCTTGT CGGGGAGCGC TAAGCATGCG ACGGCCCTAG 2100
 AGTCCCTAAC GCTCGGTTGC CGCCGGGCGT TTTTATTGT TAA 2143

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 237 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
	-23			-20					-15					-10		
5	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	
				-5					1				5			
	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
			10					15					20			
	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	
			25					30					35			
10	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	
			40					45					50			
	Thr	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	
			55					60					65			
15	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
			70					75					80			
	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Pro	Thr	
			85					90					95			
	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	
			100					105					110			
20	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	
			115					120					125			
	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
			130					135					140			
25	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
			145					150					155			
	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
			160					165					170			
	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
			175					180					185			
30	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	
			190					195					200			
	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
			205					210				214				

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: Amino Acid

5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 -23 -20 -15 -10
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
 10 -5 1 5
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 10 15 20
 Ala Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Met His Trp Met
 25 30 35
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Asn
 15 40 45 50
 Pro Lys Asn Gly Gly Thr Ser His Asn Gln Arg Phe Met Asp Arg
 55 60 65
 Phe Thr Ile Ser Val Asp Lys Ser Thr Ser Thr Ala Tyr Met Gln
 20 70 75 80
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Trp Arg Gly Leu Asn Tyr Gly Phe Asp Val Arg Tyr Phe Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
 25 115 120 125
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 130 135 140
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 30 145 150 155
 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 160 165 170
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr

175

180

185

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
190 195 200

5 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
205 210 215

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
220 225 230

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys
235 240 245

10 Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His
250 255 260

Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
265 270 275 277